

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 18, 2001, 15:30:02 ; Search time 46.42 Seconds  
(without alignments)  
745.007 Million cell updates/sec

Title: US-09-653-755A-4

Perfect score: 2427

Sequence: 1 EVQLQSGPELVKPGASVMI.....RHEGLKNVYLKTKTISRSPGK 454

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR:68:\*  
2: pir1:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### \*SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2190.5	90.3	474	1 G2MS11	Ig gamma-2b chain
2	2135	88.0	475	2 S01321	Ig gamma-2b chain
3	1835	75.6	469	2 S37483	Ig gamma-2a chain
4	1832.5	75.5	446	2 S40295	Ig gamma-2a chain
5	1797	74.0	405	1 G2MSBM	Ig gamma-2b chain
6	1439	59.3	444	2 PC4436	monoclonal antibody
7	1419	58.5	330	1 G2MSA	Ig gamma-2a chain
8	1414	58.3	399	1 G2MSAM	Ig gamma-2a chain
9	1385.5	57.1	335	1 G2MSAB	Ig gamma-2a chain
10	1326.5	54.7	333	2 PS0018	Ig gamma-2b chain
11	1321.5	54.4	472	2 S31459	Ig gamma-1 chain
12	1286.5	53.0	470	2 S22080	Ig heavy chain pre
13	1202.5	49.5	329	2 S00847	Ig gamma-2b chain
14	1170	48.2	329	1 G3MSC	Ig gamma-3 chain C
15	1159	47.8	398	1 G3MSM	Ig gamma-3 chain C
16	1150	47.4	324	1 G1MS	Ig gamma-1 chain C
17	1145	47.2	393	1 G1MSM	Ig gamma-1 chain C
18	1112	45.8	326	2 PS0017	Ig gamma-1 chain C
19	1100	45.3	330	2 PS0019	Ig gamma-1 chain C
20	1087	44.8	332	1 GHU	Ig gamma-1 chain C
21	1080.5	44.5	323	1 GHRB	Ig gamma-1 chain C
22	1080.5	44.5	329	1 G2BP	Ig gamma-2 chain C
23	1072.5	44.2	377	2 A60764	Ig gamma-3 chain C
24	1072.5	44.2	377	2 A23511	Ig gamma-3 chain C
25	1059	43.6	326	1 G2HU	Ig gamma-2 chain C
26	1058	43.6	327	1 I47159	Ig gamma-2 chain C
27	1054.5	43.4	327	1 G4HU	Ig gamma-4 chain C
28	1049	43.2	328	2 I47160	Ig gamma-2b chain
29	1028	42.4	328	2 I47161	Ig gamma-3 chain C

30	1023.5	42.2	308	2 C30554	Ig heavy chain C r
31	1022	42.1	328	2 I47158	Ig gamma 1 chain c
32	1014.5	41.8	246	2 S38950	Ig gamma chain - m
33	1008.5	41.6	348	2 S38864	Ig epsilon chain C
34	987.5	40.7	327	2 S06611	Ig gamma-2 chain C
35	918.5	37.8	374	2 S69339	Ig heavy chain V r
36	884	36.4	277	2 I47162	Ig gamma 4 chain c
37	855.5	35.2	231	2 PC4155	Ig gamma-2b chain c
38	819	33.7	549	2 S04845	Ig heavy chain pre
39	818.5	33.7	627	2 S14683	Ig mu chain precu
40	781.5	32.2	255	4 S31866	Ig gamma-1 chain C
41	778.5	32.1	221	2 S49220	Ig gamma-1 chain -
42	778	32.1	214	2 PC4202	monoclonal antibody
43	774.5	31.9	213	2 S68213	Ig heavy chain (Ma
44	774.5	31.9	234	2 PT0207	Ig gamma chain C r
45	771.5	31.8	289	1 G3H0W1	Ig gamma-3 heavy c

#### ALIGNMENTS

RESULT 1  
G2MS11  
Ig gamma-2b chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Mar-1980 #sequence\_revision 01-Dec-2000 #text\_change 01-Dec-2000  
C:Accession: S25057; A02157; A26235; A26232; A26233; A53598  
R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.  
Submitted to the EMBL Data Library, July 1992  
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific  
A:Reference number: S25057  
A:Accession: S25057  
A>Status: Preliminary  
A:Residues: 1-474 <FIS>  
A:Molecule type: mRNA  
R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Odate, M.; Honjo, T.  
Nature 283, 786-789, 1980  
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned fro  
A:Reference number: A02157; MUID:80120716  
A:Contents: a allele  
A:Accession: A02157  
A:Molecule type: DNA  
A:Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>  
A:Cross-references: GB:J00461  
A:Note: the sequence was determined from the germline gene  
R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.  
Science 206, 1299-1303, 1979  
A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b  
A:Reference number: A26235; MUID:80081501  
A:Contents: MPC 11  
A:Accession: A26235  
A:Molecule type: mRNA  
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU>  
A:Note: Lys-474 is probably removed posttranslationally  
R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.  
Science 206, 1303-1306, 1979  
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immuno  
A:Reference number: A26232; MUID:80081502  
A:Accession: A26232  
A:Molecule type: DNA  
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU>  
R:Ollo, R.; Rougeon, F.  
Nature 296, 761-763, 1982  
A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and g  
A:Reference number: A26233; MUID:82173203  
A:Contents: b allele  
A:Accession: A26233  
A:Molecule type: DNA  
A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OL  
A:Cross-references: GB:J00461  
R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takah  
J. Biol. Chem. 269, 12345-12350, 1994

A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.  
A:Reference number: A53598; MUID:94216359  
A:Accession: A53598  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 234-251 <KIM>  
C:Comment: The a allele sequence is shown.  
C:Genetics:  
A:Introns: 138/1; 236/1; 258/1; 368/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a C:Superfamily: Immunoglobulin C region; Immunoglobulin homology  
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin  
F:157-222/Domain: immunoglobulin homology <IM1>  
F:236-257/Region: hinge  
F:281-350/Domain: immunoglobulin homology <IM2>  
F:387-454/Domain: immunoglobulin homology <IM3>  
F:152/Disulfide bonds: interchain (to light chain) #status predicted  
F:164-220,288-348,394-452/Disulfide bonds: #status predicted  
F:247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted  
F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 90.3%; Score 2190.5; DB 1; Length 474;  
Best Local Similarity 91.2%; Pred. No. 1.4e-123;  
Matches 415; Conservative 10; Mismatches 29; Indels 1; Gaps 1;  
QY 1 EVOLQSGELVPGASVWISCRSAFTFTENTVHWKSHGSLWIGINPYGGSIF 60  
DB 20 EVOLQSGELVPGASVWISCRSAFTFTENTVHWKSHGSLWIGINPYGGSIF 79  
QY 61 SPKFKGKATLVYDKSSSTAYMELSLTSDSAVYCARAGAYFDYWGQGLTVYSSAK 120  
DB 80 NEFKGKATLVYDKSSSTAYMELSLTSDSAVYCARAGAYFDYWGQGLTVYSSAK 139  
QY 121 TRPPSYPLAPGCGDTGSSVTLGCLVKGFPESVTVTNMNSGSLSSVHTF-PALLQSGI 179  
DB 140 TRPPSYPLAPGCGDTGSSVTLGCLVKGFPESVTVTNMNSGSLSSVHTF-PALLQSGI 199  
QY 180 YTMSSSVTPSSVTPSQVTCVAHPASTVYDKLEPSPGISTINPCPKCKCHKCPA 239  
DB 200 YTMSSSVTPSSVTPSQVTCVAHPASTVYDKLEPSPGISTINPCPKCKCHKCPA 259  
QY 240 NEEGSPVFIFPPNIKDVLMISLTPKVTGVVVDSEDDPVOISFVNNVEVHTAQTQTH 299  
DB 260 NEEGSPVFIFPPNIKDVLMISLTPKVTGVVVDSEDDPVOISFVNNVEVHTAQTQTH 319  
QY 300 REDYNTIVVSTLPIQHODMMSGKEFKCKVNNKDLPSPIERTISKIGLVAPQVYILP 359  
DB 320 REDYNTIVVSTLPIQHODMMSGKEFKCKVNNKDLPSPIERTISKIGLVAPQVYILP 379  
QY 360 PRAEQLSRKDVSLTCLVGFNPGDISVEMTNGHTEENKDTAPVLDSDGSYFTSKLN 419  
DB 380 PRAEQLSRKDVSLTCLVGFNPGDISVEMTNGHTEENKDTAPVLDSDGSYFTSKLN 439  
QY 420 KTSKWEKTDSCNVRHGLKNYLLKKTISRSPGK 454  
DB 440 KTSKWEKTDSCNVRHGLKNYLLKKTISRSPGK 474

RESULT 2  
S01321  
Ig gamma-2b chain precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 23-Jul-1999  
C:Accession: S01321  
R:de Waele, P.; Ferys, V.; van de Voorde, A.; Molmans, F.; Fiers, W.  
Eur. J. Biochem. 176, 287-295, 1988  
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed at  
A:Reference number: S01320; MUID:88329081  
A:Accession: S01321  
A:Molecule type: mRNA  
A:Residues: 1-475 <DEI>

A:Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781  
A:Note: this sequence was determined from the differentiated gene  
C:Superfamily: Immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-475/Product: Ig gamma-2b chain #status predicted <KAT>  
F:159-223/Domain: immunoglobulin homology <IMX>

Query Match 88.0%; Score 2135; DB 2; Length 475;  
Best Local Similarity 88.4%; Pred. No. 3e-120;  
Matches 403; Conservative 15; Mismatches 36; Indels 2; Gaps 1;  
QY 1 EVOLQSGELVPGASVWISCRSAFTFTENTVHWKSHGSLWIGINPYGGSIF 60  
DB 20 EVOLQSGELVPGASVWISCRSAFTFTENTVHWKSHGSLWIGINPYGGSIF 79  
QY 61 SPKFKGKATLVYDKSSSTAYMELSLTSDSAVYCARAGAYFDYWGQGLTVYSS 118  
DB 80 NEFKGKATLVYDKSSSTAYMELSLTSDSAVYCARAGAYFDYWGQGLTVYSS 139  
QY 119 AKTTPSYPLAPGCGDTGSSVTLGCLVKGFPESVTVTNMNSGSLSSVHTFPALLQSG 178  
DB 140 AKTTPSYPLAPGCGDTGSSVTLGCLVKGFPESVTVTNMNSGSLSSVHTFPALLQSG 199  
QY 179 LYTMSSSVTPSSVTPSQVTCVAHPASTVYDKLEPSPGISTINPCPKCKCHKCPA 238  
DB 200 LYTMSSSVTPSSVTPSQVTCVAHPASTVYDKLEPSPGISTINPCPKCKCHKCPA 259  
QY 239 PNEEGSPVFIFPPNIKDVLMISLTPKVTGVVVDSEDDPVOISFVNNVEVHTAQTQTH 298  
DB 260 PNEEGSPVFIFPPNIKDVLMISLTPKVTGVVVDSEDDPVOISFVNNVEVHTAQTQTH 319  
QY 299 HREDYNTIVVSTLPIQHODMMSGKEFKCKVNNKDLPSPIERTISKIGLVAPQVYIL 358  
DB 320 HREDYNTIVVSTLPIQHODMMSGKEFKCKVNNKDLPSPIERTISKIGLVAPQVYIL 379  
QY 359 PRAEQLSRKDVSLTCLVGFNPGDISVEMTNGHTEENKDTAPVLDSDGSYFTSKLN 418  
DB 380 PRAEQLSRKDVSLTCLVGFNPGDISVEMTNGHTEENKDTAPVLDSDGSYFTSKLN 439  
QY 419 KTSKWEKTDSCNVRHGLKNYLLKKTISRSPGK 454  
DB 440 KTSKWEKTDSCNVRHGLKNYLLKKTISRSPGK 475

RESULT 3  
S37483  
Ig gamma-2a chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S37483  
R:Ducancel, F.F.D.  
submitted to the EMBL Data Library, February 1993  
A:Reference number: S37483  
A:Accession: S37483  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-469 <DUC>  
A:Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA9868.1; PID:g406253  
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology  
C:Keywords: immunoglobulin  
F:276-345/Domain: immunoglobulin homology <IMX>

Query Match 75.6%; Score 1835; DB 2; Length 469;  
Best Local Similarity 75.7%; Pred. No. 2.2e-102;  
Matches 345; Conservative 44; Mismatches 59; Indels 8; Gaps 3;  
QY 1 EVOLQSGELVPGASVWISCRSAFTFTENTVHWKSHGSLWIGINPYGGSIF 60  
DB 20 EVOLQSGELVPGASVWISCRSAFTFTENTVHWKSHGSLWIGINPYGGSIF 79

[illegible]

Oy	121	TTTTPEVYVLAAGCGGTTGSSVTLGCLVYKGPRESVETVYMMNNGSLSSSSHHPPALLOGLY	180
Dd	120	TTABSVITFLAPACGGTJTGSSVTLGCLVYKGPITPEPPTLLWMSGSLSSGHHTPVALDOSLY	179
Oy	181	TMSSSVTPPSSSTWPSQOTYTCGSVANHASSSTYDCKLEPSGPISTINPCSPCKECHKCAPN	240
Dd	180	TLSSSVVYTTSSWPSQOSTITCNVHAPASSTYKDKTIERGPR--TIKPCPRG---KCAPN	233
Oy	241	LEGGESVFIIPPNIKIDVLMISLTPEKVTGVVVVDSEDDPDVQISMFVNNEVHTAOTQOTHR	300
Dd	234	LLGGESVFIIPPNIKIDVLMISLTPEWTCVVVDSEDDPDVQISMFVNNEVHTAOTQOTHR	293
Oy	301	EDYNSTIRVYSLTPLOHODMMSGKFEKCKVANNKDLPSITERTISKIGLVAPAYUILLP	360
Dd	294	EDYNSTIRVYSLTPLOHODMMSGKFEKCKVANNKDLPAEIERTISKPKSVAPAYUILLP	353
Oy	361	PAEOLSRDVSILTCVYVAFNPGDISVENTSGNHTPEENKDPAPVLDOSGSFYITSKLNMK	420
Dd	354	PEEETKQVYLTICAVTDFMPREDIYVENTNGNKTELNTKNEPVALDOSGSFYITSKLRAVE	413
Oy	421	TSKWEKTSFSCGNVHNEGILKNVYLKKTITSRSPG	453
Dd	414	KNWERNSTYSGSVVHEGLNHNHTTKSFSPRPG	446

[illegible]

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RESULT 5
G2MSBM
Ig gamma-2b chain C region, membrane-bound form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 17-Dec-1992 #sequence,revision 31-Mar-1991 #text,change 16-Jul-1999
C:Accession: C02154; A02158; B02157
R:Yamawaki-Kataoka, Y.; Nakai, S.; Miyata, T.; Honjo, T.
Proc. Natl. Acad. Sci. U.S.A. 79, 2623-2627, 1982
A:Title: Nucleotide sequences of 9c gene segments encoding membrane domains of immunoglobulin
A:Reference number: A02154; MUID:82222190
A:Accession: C02154
A:Molecule type: DNA
A:Residues: 335-405 <YAM>
A:Cross-references: GB:J00462
R:Rogers, J.; Choi, E.; Souza, L.; Carter, C.; Word, C.; Kuehl, M.; Eisenberg, D.; Wall
Cell 26, 19-27, 1981
A:Title: Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma
A:Reference number: A02158; MUID:82115295
A:Accession: A02158
A:Molecule type: DNA
A:Residues: 335-378 <ROG>
A:Note: The translation of the first exon of the membrane-bound segment is given
R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obara, M.; Honjo, T.
Nature 283, 786-789, 1980
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from
A:Reference number: A02157; MUID:80120716
A:Contents: a allele
A:Accession: B02157
A:Molecule type: DNA
A:Residues: 1-335,'K' <YA2>
C:Comment: The sequence of residues 1-334 was assumed to be identical with the corres
C:Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The
hat it contains an alternative 3' end, encoded in separate exons, that is homologous
C:Genetics:
A:Introns: 1/1; 98/1; 120/1; 230/1; 335/1; 378/3
A:C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (L)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: Immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunogl
F:143-212/Domains: immunoglobulin homology <IMM>
F:352-369/Domains: transmembrane #status predicted <TM>
F:370-405/Domains: intracellular #status predicted <INT>
F:186/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 74.0%; Score 1797; DB 1; Length 405;
Best Local Similarity 100.0%; Pred. No. 3, 5e-100;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	119	AKTTPPSVYPLA	PGGDDTSSVTG	CLVKYGFPSVATV	WNMSSGLSSVHF	PALLDSG	178
Db	1	AKTTPPSVYPLA	PGGDDTSSVTLG	CLVKYGFPSVATV	WNMSSGLSSVHF	PALLDSG	60
QY	179	LYTMSSSVTVBS	STPISQTVTC	SVAHPASSTV	VDKLEPSGPIST	INPCPCKECHKCPA	238
Db	61	LYTMSSSVTVBS	STPISQTVTC	SVAHPASSTV	VDKLEPSGPIST	INPCPCKECHKCPA	120
QY	239	PNLEGGPSVF	TFPPNIKDVLMISL	TPKVTQVVDV	SEDDPDVQISMF	VNNVEVHTAQOT	298
Db	121	PNLEGGPSVF	TFPPNIKDVLMISL	TPKVTQVVDV	SEDDPDVQISMF	VNNVEVHTAQOT	180
QY	299	HREDYNSITR	IVAVSTLPI	IOHODM	SGKEFKCV	NNKDLPSPIERTTSKIKGLV	RAQVYIL 358
Db	181	HREDYNSITR	IVAVSTLPI	IOHODM	SGKEFKCV	NNKDLPSPIERTTSKIKGLV	RAQVYIL 240
QY	359	PPPAEOLSR	KVYSLTLC	LVVGFNP	GDISVEWTS	NGHTEENYKDTA	VLDSDSGSYFIYSKLN 418
Db	241	PPPAEOLSR	KVYSLTLC	LVVGFNP	GDISVEWTS	NGHTEENYKDTA	VLDSDSGSYFIYSKLN 300
QY	419	MKTSKWEK	TDSFSCNV	RHEGLKNY	LKKTISR	SPG 453	
Db	301	MKTSKWEK	TDSFSCNV	RHEGLKNY	LKKTISR	SPG 335	

RESULT 6  
PC4436  
monoclonal antibody 13-1 heavy chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jan-2000  
C:Accession: PC4436  
R:Ashish, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.  
Biochem. Biophys. Res. Commun. 240, 566-572, 1997  
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin  
A:Reference number: JCS810; MUID:98063277  
A:Accession: PC4436  
A:Molecule type: protein  
A:Residues: 1-444 <AKA>  
C:Comment: This catalytic antibody has peroxidase oxidase activity. It is directed against  
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology  
F:251-320/Domain: Immunoglobulin homology <IMM>  
F:22/Disulfide bonds: Interchain (to 98) #status predicted  
F:99/Disulfide bonds: Interchain (to 109) #status predicted

Query Match	59.3%;	Score 1439;	DB 2;	Length 444;
Best Local Similarity	59.3%;	Pred. No. 8.5e-79;		
Matches 271;	Conservative 68;	Mismatches 102;	Indels 16;	Gaps 6

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OY      1 EVOLQOOSPELVKLGASVWISCRTSAVYFTENTVWVWQSGESLEWJGGI---NPYQG  57
OY      1 EVQAVETGCGLVGRGNLSKLKLSCLTSGFTFSYRHHMLFQPGKRLKLEIAVITVKSNDYGA  60
OY      58 SIFSPKEGKATLTVDKSSSTAYMELRSLTSDSAVYVCARAGAYPYEDYGOGTTLTVS  117
OY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  118
OY      K-YAESVGRGRTISBDKSSVYLQMNRLREDGATATYCCGTPWYAMDCKGQGSVAYS  119
OY      61
OY      118 SAKTTPSVVYLABGCGDTGSSVTLGCLVKGYPESVYTVWNSGLSSSVHTPEALLQS  177
OY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  178
OY      120 SAKTTPSVVYLABGSAAQOTNSWTLGCLVKGYPEPYTVWNSGLSSGHTPEAVLQS  179
OY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  180
OY      178 GLTYMSSSVYVPSSTWPSQVITCSVAHPASSTVYDKLKEBGPSTINPCPCKECKHCP  237
OY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  238
OY      180 DLYTLSSSVYVPSSTWPSSEIVTCNVAHPASSTKVDKILVP-----RDC-GCKPCC-ICT  230
OY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  231
OY      238 APNLEGGSVYIEFPNPKDVLMLISLTPKVCVVYDVSDDDDDVQISMVNNVVEVHTAQO  297
OY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  298
OY      231 VPES-----SVIEFPKRPDVLITLTPKVCVVYDVSDKDDDEVQFSWVDVDEVHTAQO  287
OY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  288
OY      298 THRDYNSITRVSYTLPIODHMMSGKEFKCVNNKDLPSPIERTISKIKGLVAPQYI  357
OY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  358
OY      288 PREQGFNSTRSVSELPIMODMLNGKEFKCVNNSAAPAIETKTIISTKTRPAPQYTT  347

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[illegible]

RESULT	7
G2MSA	

Ig gamma-2a chain C region, secreted form (allele a) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Sep-1980 #sequence\_revision 01-Sep-1981 #text\_change 16-Jun-2000  
C:Accession: A02152; A32657; A32658  
R:Sikarov, J.L.; Aufitray, C.; Rougeon, F.  
Nucleic Acids Res. 8, 3143-3155, 1980  
A>Title: Structure of the constant and 3' untranslated regions of the murine Balb/C g

A:Reference number: A02152; MUID:81076554  
A:Accession: A02152  
A:Molecule type: mRNA  
A:Residues: 1-330 <STK>  
A:Cross-references: GB:V00798; NID:g51835; PIDN:CAA24178..1; PID:g1333984  
R.Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T.  
Nucleic Acids Res. 9, 1365-1381, 1981  
A>Title: The complete nucleotide sequence of mouse immunoglobulin gamma 2 A gene and  
A:Reference number: A32657; MUID:81198976  
A:Accession: A32657  
A:Molecule type: DNA  
A:Residues: 1-330 <YAM>  
A:Cross-references: GB:J00470  
A>Note: the sequence was determined from the germline gene  
R.Ollo, R.; Aufitray, C.; Morchamps, C.; Rougeon, F.  
Proc. Natl. Acad. Sci. U.S.A. 78, 2442-2446, 1981  
A>Title: Comparison of mouse immunoglobulin gamma-2A and gamma-2B chain genes suggeste  
A:Reference number: A32658; MUID:81223894  
A:Accession: A32658  
A:Molecule type: DNA  
A:Residues: 1-330 <OLL>  
A>Note: the sequence was determined from the germline gene  
A>Note: Lys-330 is removed posttranslationally  
R.Bourgois, A.; Fougerau, M.; Rocca-Serra, J.  
Eur. J. Biochem. 43, 423-435, 1974  
A>Title: Determination of the primary structure of a mouse IgG2a immunoglobulin: amin  
A:Reference number: A32659; MUID:74175517  
A:Contents: annotation; myeloma protein MOPC 173  
A>Note: this is one paper in a series reporting the sequence; for additional reference  
A>Note: this sequence differs from that shown at a number of positions  
R.de Preval, C.; Fougerau, M.  
Eur. J. Biochem. 30, 452-462, 1972  
A>Title: Determination of the primary structure of a mouse gammaG2a immunoglobulin. I  
A:Reference number: A32660; MUID:73056887  
A:Contents: annotation; MOPC 173, disulfide bonds  
C:Genetics:  
F:Introns: 1/1; 98/1, 114/1; 224/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (L  
Chain: disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into  
Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunogl  
F:20-84/Domain: immunoglobulin homology <IM1>  
F:98-113/Region: hinge  
F:137-206/Domain: immunoglobulin homology <IM2>  
F:243-310/Domain: immunoglobulin homology <IM3>  
F:15/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-82,144-204,250-308/Disulfide bonds: #status experimental  
F:107,110,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:180/Binding site: carbohydrate (Asn) (covalent) #status predicted

	Query Match	Best Local Similarity	Matches
	58.5%	Score 1419; DB 1;	Length 330;
	78.6%;	Pred. No. 9,4e-78;	
	30;	Mismatches 36;	Indels 6; Gaps 2;

[illegible]

Blast Local Similarity 78.5%; Pred. No. 2,36-77;  
Matches 263; Conservative 30; Mismatches 36; Indels 6; Gaps 2;

OY 119 AKTTPPSVYLAPAGCGDITGSSVTLCGLVKGYFPESAVTVTNWSGSLSSSVHTFPAALQSG 178  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 1 AKTAPASVYPLAPVCGDTGGTSSTVLGCGLVKGFPEPPTL/TMWSGSLSGVHTEFAVLQSD 60

OY 179 LYTMSSTVTVBSSTMPSQTCVAHPASSITTVDKKLEPSPGISITINCPCKECKKCPA 238  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 61 LYTLSSSYTVNISTWPDSOSITCNVAHPASSITFKDKKIEPRGP--TIKPCPP---KCBA 114

OY 239 PRLGGPGVFEPPIPKIVMLMTSLPKYTCVVYDVSEDDPDVOISMFNVNVEVHAQTOT 298  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 115 PLLLGPGPVFFIPPKIKDVMLTSLPIVTCVADVSEDDPDOVISMFVNNEVHTAQRT 174

OY 299 HREDNSTIRVYSTLPIDIOHDMMSGKEFEKCAKNNDLPSIPTERTISKIGLVRAPOVIL 358  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 175 HREDNSTLRVSVALPIQHODMMASKERKCYANNKDLPAPIERTISKRGSAQAQYYVL 234

OY 359 PPBAPOLSRKDYSLTCLVGVGNPDGI SVEMWTNGHEENYKDFAPVLDSDGSYFLSKLN 418  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 235 PPPEEPMRKQYTLCTCMVTD FMPEDIVYEWNNGKTELNYKTBEPLVLDSDGSYFMYSKL R 294

OY 419 MKTSKWERTDSCSNVRHDEGLKNLYLKTTISNSPG 453  
:: : ::  
Db 295 VEKKNWERNYSYCSVHEGLMHNHTTKFSKPTG 329

RESULT 9

G2MSAB

Ig gamma-2a chain C region, secreted form (allele b) - mouse

C:Species: Mus musculus (house mouse)

C:date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 16-Jul-1999

C:Accession: A02153; A32656

R:Schreier, P.H.; Botwell, A.L.M.; Mueller-Hill, B.; Baltimore, D.

A:Title: Multiple differences between the nucleic acid sequences of the IgG2a(a) and

A:Reference number: A02153; MUID:82037861

A:Accession: A02153

A:Molecule type: mRNA

A:Residues: 1-335 <SCH>

A:Cross-references: GB:J00479

A:Experimental source: strain C57BL/6

R:Dognin, M.J.; Lauwereys, M.; Strosberg, A.D.

Proc. Natl. Acad. Sci. U.S.A. 78, 4031-4035, 1981

A:File: Multiple amino acid substitutions between murine gamma 2a heavy chain FC reg

A:Reference number: A32656; MUID:82037777

A:Accession: A32656

A:Molecule type: Protein

A:Residues: 118-267,'E','269-328,'G','330-334 <DOG>

C:Comment: Lys-335 is removed posttranslationally.

C:Comment: The sequence differs from that of the a allele, from BALB/c mice, at 15% c

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (c

C:chain disulfide bonds. In some cases, such as Iga and IgM, the subunits associate inte

C:Superfamily: Immunoglobulin C region; immunoglobulin homology

C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunog

F:20-84/Domain: immunoglobulin homology <IM1>

F:98-118/Region: hinge

F:142-211/Domain: immunoglobulin homology <IM2>

F:248-315/Domain: immunoglobulin homology <IM3>

F:15/Disulfide bonds: Interchain (to light chain) #status predicted

F:27-82,149-209,253-313/Disulfide bonds: #status predicted

F:108-117/Disulfide bonds: Interchain (to heavy chain) #status predicted

F:185/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 57.1%; Score 1385.5; DB 1; Length 335;  
Best Local Similarity 77.1%; Pred. No. 9,5e-76;  
Matches 259; Conservative 33; Mismatches 43; Indels 1; Gaps 1;

OY 119 AKTTPPSVYLAPAGCGDITGSSVTLCGLVKGYFPESAVTVTNWSGSLSSSVHTFPAALQSG 178  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 1 AKTAPASVYPLAPVCGDTGGTSSTVLGCGLVKGFPEPPTL/TMWSGSLSGVHTEFAVLQSG 60

Oy	179	LYTMSSTVYSSVMPISOTVYCSVAHBAASSTVYDKLEBPGPSTINPCOPCKECHKCA	238
Oy	179	LYTMSSTVYSSVMPISOTVYCSVAHBAASSTVYDKLEBPGPSTINPCOPCKECHKCA	238
Db	61	LXTLSSTVYSSVMPISOTVYCSVAHBAASSTVYDKLEBPGPSTINPCOPCKECHKCA	119
Oy	239	PNEGGPSVFTFPPIKDVIMISLTPKRYTCVYVDSSEDDPVOISFVNNVYEHNTAQOT	298
Db	120	PDLGGPSVFTFPPIKDVIMISLTPKRYTCVYVDSSEDDPVOISFVNNVYEHNTAQOT	179
Oy	299	HREDYNSIRVYSLPLIOHODMMSGKRFCKKVVNNKOLPSPTEPTIKIGIYVAPVYTL	358
Oy	299	HREDYNSIRVYSLPLIOHODMMSGKRFCKKVVNNKOLPSPTEPTIKIGIYVAPVYTL	358
Db	180	HREDYNSIRVYSLPLIOHODMMSGKRFCKKVVNNKOLPSPTEPTIKIGIYVAPVYTL	239
Oy	359	PPPAEQLSRKDVSLTCLVGFNPBGDISVENTSGHTEENKKTAPVYLDGSGSYFTISKLN	418
Db	240	PPPAEQLSRKDVSLTCLVGFNPBGDISVENTSGHTEENKKTAPVYLDGSGSYFTISKLN	299
Oy	419	MKTSKWEKTDSCNVNHEGLKNYLLKKTISRSBGRK	454
Db	300	VOKSTWEGSLFACSVYVHEVHNHNLTTTKTISRSISGRK	335

## RESULT 10

Ig gamma-2b chain C region - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 16-Jul-1999  
C:Accession: PS0018; B25941  
R:Bruggemann, M.  
Gene 74, 473-482, 1988  
A:Title: Evolution of the rat immunoglobulin gamma heavy-chain gene family.  
A:Reference number: PS0017; MUID:89232738  
A:Accession: PS0018  
A:Molecule type: DNA  
A:Residues: 1-333 <BRU>  
R:Bruggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.  
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986  
A:Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibody  
A:Reference number: A25941; MUID:86287397  
A:Accession: B25941  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 227-333 <BR2>  
C:Genetics:  
A:Introns: 96/1; 117/1; 227/1  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
;20-82/Domain: immunoglobulin homology <IMM>

Query Match	Similarity	54.7%	Score 1326.5	DB 2	Length 333
Best Local	Similarity	73.6%	Pred. No. 3.1e-72		
Matches	Conservative	34	Mismatches	50	Indels
					Gaps
QY	119	AKTTPSVYPLAPGCGDITTSVTGICLVKGYEPESVATYTNMGSLSSTSVHFFPALLOSG	178		
Db	1	AQTTPSVYPLAPGCGDITTSVTGICLVKGYEPESVATYTNMGSLSSTSVHFFPALLOSG	60		
QY	179	LYTMSSVTVSSVTSMPQSTQVTCNVAPASSTVVDKLE-PSGPSTINPCPECKECHKP	237		
Db	61	LYTLTSSVT--SSTMPQSTQVTCNVAPASSTVVDKKEVERNGIG--HKCPCPCHCHKP	116		
QY	238	APNLEGGSVLEFPPIKDVLMISLPKPYCVVVDSEDDPDVQISWFNVNYEHTAQO	297		
Db	117	VPLELGGSVLEFPKPKDILLISQNAKVTYCVVDVSEEDPDVQSWFNNYEHTAQO	176		
QY	298	THREDYNTIRVSTLPIOHODMMSGKEFKCKVNNKDLSPLEPITISIKGLVRAPOYIT	357		
Db	177	PREQDYNSTFRVSAALPIOHODMMSGKEFKCKVNNKALSPLEKTIISKPKGLVRPOYV	236		
QY	358	LPPAPEQISRRDYSITCLVGNFPGDIDYEWMSNGHTEENYKDTAPAVLSDOSYITISKL	417		
Db	237	MGPPPEQLTEQDVTSLTCLTSGFLPNDIEGWTISNHIKNNKNTPEVVDSDSFFMYISL	296		

```
Oy      418 NMKTSKEWETDSFSCNVRHEGLKNLYLKTITSRSPGK 454  
         |::|::|::|::|::|::|::|::|::|::|::|  
Db      297 NVERSRWDRAFPVCSVVHGGJLNHHVEKSISRPPGK 333
```

## RESULT 11

Ig gamma-1 chain - sheep (fragment)  
C:Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 16-Jul-1999  
A:Accession: S31459  
R:Patrl, S.; Nau, F.  
submitted to the EMBL Data Library, December 1992  
A:Reference number: S31459  
A:Accession: S31459  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-472 <P>  
A:Cross-references: EMBL:X69797  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
:277-346/Domain: immunoglobulin homology <IMM>  
:277-346/Domain: immunoglobulin homology

Query Match

[illegible]









